

SEQUENCE LISTING TABLE

The sequences referred to in the specification above are provided in the following table.

5	SEQ ID NO: 1	5'-CATTCTAGAACCTCGACAAGCTTGAGATCACAGTTCTCTCTAC-3'
	SEQ ID NO: 2	5'-CAGCAGGCTGGGOCACGTGCATTGCGGAGTGGACACCTGTGGAGAG-3'
10	SEQ ID NO: 3	5'-CTCTCCACAGGTGTCCACTCCGCAATGCACGTGGCCCAGCCTGCTG-3'
	SEQ ID NO: 4	5'-TGTGTGTGGAATTCTCATTACTGATCAGAATCTGGGCACGGTTCTG-3'
15	SEQ ID NO: 5	5'-GCATTTTAAGCTTTTCCTGATCAGGAGCCCAAATCTTCT GACAAAACCTCACACATCTCCACCGTCTCCAGGTAAGCC-3'
20	SEQ ID NO: 6	5'TAATACGACTCACTATAGGG-3'
	SEQ ID NO: 7	5'GAGCATTTTCCTGATCAGGAGTCCAAATATGGTCCCCCACCCC ATCATCCCCAGGTAAGCCAACCC-3'
25	SEQ ID NO: 8	5'GCAGAGGAATTCGAGCTCGGTACCCGGGGATCCCCAGTGTGGGG ACAGTGGGACCCGCTCTGCCTCCC-3'
30	SEQ ID NO: 9	5'-GGGTTTTGGGGGAAGAGGAAGACTGACGGTGCCCCCTCGGCTT CAGGTGCTGAGGAAG-3'
35	SEQ ID NO: 10	5'-CATCTCTTCCTCAGCACCTGAAGCCGAGGGGGCACCGTCAGTCT TCCTCTTCCCCC-3'

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REMOVED BY ATTCN
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SEQ ID NO: 11 5'-CGCACGTGACCTCAGGGGTCCGGGAGATCATGAGAGTGTCTTG
GGTTTTGGGGGAACAGGAAGACTGATGGTGCCCCCTCGAACTCAG GTGCTGAGG-3'

5 SEQ ID NO: 12 5'-CCTCAGCACCTGAGTTCGAGGGGGCACCATCAGTCTTCCTGTTCCC
CCCCAAACCCAAGGACACTCTCATGATCTCCCGGACCCCTGAGGTCA CGTGCG-3'

SEQ ID NO: 13
5'CATTGCTTACCTCGACAAGCTTGAGATCACAGTTCTCTCTAC-3'

10 SEQ ID NO: 14
5'-GGAGTGGACACCTGTGGAGAG-3'

15 SEQ ID NO: 15
5'-CTCCACAGGTGTCCACTCCGCAATGCACGTGGCCCAGCC-3'

SEQ ID NO: 16
5'GAGGTTGTAAGGACTCACCTGAAATCTGGGCTCCGTTGC-3'

20 SEQ ID NO: 17
5'-GCAACGGAGCCCAGATTTCAGGTGAGTCCTTACAACCTC-3'

SEQ ID NO: 18
5'-GGCTAGATATCTCTAGACTATAAATCTCTGGCCATGAAG-3'

25 SEQ ID NO: 19
5'-GGCACTAGGTGACTCTAGAACTGAGGAAGCAAAGTTTAAATTCTAC
TCACGTTTAATCTGGGCTCCGTTGC-3'

30 SEQ ID NO: 20
5'GCAGAGAGACATATGGCAATGCACGTGGCCCAGCCTGCTGTGG-3'

SEQ ID NO: 21
5'-GCAGAGAGAGGATCCTCAGTCAGTTAGTCAGAATCTGGGCACGGTT
CTGG-3'

35 SEQ ID NO: 22
5'-GGCACTAGTCATGAAATACCTATTGCCTACGGCAGCCGCTGGA
TTGTTATTACTCGCTGCCCAACCAGCGATGGCCGAGCAA

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TGCACGTGGCCCAGCCTGCTGTGG-3'

SEQ ID NO: 23

5 1 CATTTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT
51 GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG
10 101 TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA
151 CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG
201 TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC
15 251 CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC
301 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG
20 351 TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT
401 TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA
451 AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA
25 501 TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT
551 GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGC CCAAATCTTC
30 601 TGACAAAACCT CACACATCTC CACCGTCTCC AGGTAAGCCA GCCCAGGCCT
651 CGCCCTCCAG CTCAAGGCGG GACAGGTGCC CTAGAGTAGC CTGCATCCAG
701 GGACAGGCCC CAGCCGGGTG CTGACACGTC CACCTCCATC TCTTCCTCAG
35 751 CACCTGAAGC CGAGGGGGCA CCGTCAGTCT TCCTCTTCCC CCCAAAACCC
801 AAGGACACCC TCATGATCTC CCGGACCCCT GAGGTCACAT GCGTGGTGGT
851 GGACGTGAGC CACGAAGACC CTGAGGTCAA GTTCAACTGG TACGTGGACG
40 901 GCGTGGAGGT GCATAATGCC AAGACAAAGC CGCGGGAGGA GCAGTACAAC
951 AGCACGTACC GGGTGGTCAG CGTCCTCACC GTCCTGCACC AGGACTGGCT
45 1001 GAATGGCAAG GAGTACAAGT GCAAGGTCTC CAACAAAGCC CTCCCAGCCC
1051 CCATCGAGAA AACCATCTCC AAAGCCAAAG GTGGGACCCG TGGGGTGCAG
1101 GGGCCACATG GACAGAGGCC GGCTCGGCCC ACCCTCTGCC CTGAGAGTGA
50 1151 CCGCTGTACC AACCTCTGTC CTACAGGGCA GCCCGAGAA CCACAGGTGT
1201 ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTCAGCCTG
55 1251 ACCTGCCTGG TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA

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1301 GAGCAATGGG CAGCCGGAGA ACAACTACAA GACCACGCCT CCCGTGCTGG
1351 ACTCCGACGG CTCCTTCTTC CTCTACAGCA AGCTCACCGT GGACAAGAGC
1401 AGGTGGCAGC AGGGGAACGT CTTCTCATGC TCCGTGATGC ATGAGGCTCT
1451 GCACAACCAC TACACGCAGA AGAGCCTCTC CCTGTCTCCG GGTAATGAG
1501 TGCACGCGCC GGCAAGCCCC GCTCCCCGGG CTCTCGCGGT CGCACGAGGA
1551 TGCTTGGCAC GTACCCCTG TACATACTTC CCGGGCGCCC AGCATGGAAA
1601 TAAAGCACCC AGCGCTGCCC TGGGCCCCCTG CGAGACTGTG ATGGTTCTTT
1651 CCACGGGTCA GGCCGAGTCT GAGGCCTGAG TGGCATGAGG GAGGCAGAGC
1701 GGGTC

20 SEQ ID NO:24

1 MGWSCIIILFL VATATGVHSA MHVAQPAVL ASSRGIAFV CEYASPGKAT
51 EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ
101 GLRAMDTGLY ICKVELMYPP PYYLGIGNGT QIYVIDPEPC PDSQEPKSS
151 DKHTHTSPPSP APEAEGAPSV FLFPPKPKDT LMISRTPEVT CVVVDVSHED
201 PEVKFNWYVD GVEVHNAKTK PREEQYNSTY RVVSVLTVLH QDWLNGKEYK
251 CKVSNKALPA PIEKTISKAK GQPREPQVYT LPPSRDELTK NQVSLTCLVK
301 GFYPSDIAVE WESNGQPENN YKTTTPVLDS DGSFFLYSKL TVDKSRWQQG
351 NVFSCSVMHE ALHNHYTQKS LSLSPGK*

SEQ ID NO: 25

1 CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT
51 GAGCACACAG GACCTACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG
101 TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA
151 CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG
201 TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC
251 CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC
301 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG
351 TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT

401 TCCATCTGCA CGGGCACCTC CAGTGGAAAT CAAGTGAACC TCACTATCCA
5 451 AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA
501 TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT
551 GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG
10 601 TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCAGGCC TCGCCCTCCA
651 GCTCAAGGCG GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC
701 CCAGCCGGGT GCTGACGCAT CCACCTCCAT CTCTTCCTCA GCACCTGAGT
15 751 TCCTGGGGGG ACCATCAGTC TTCCTGTTCC CCCCCAAACC CAAGGACACT
801 CTCATGATCT CCCGGACCCC TGAGGTCACG TGCGTGGTGG TGGACGTGAG
20 851 CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GCGGTGGAGG
901 TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC
951 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA
25 1001 GGAGTACAAG TGCAAGGTCT CCAACAAAGG CCTCCCGTCC TCCATCGAGA
1051 AAACCATCTC CAAAGCCAAA GGTGGGACCC ACGGGGTGCG AGGGCCACAC
30 1101 GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG ACCGCTGTGC
1151 CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG
1201 CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT
35 1251 GGTCAAAGGC TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG
1301 GGCAQCCGGA GAACAACTAC AAGACCACGC CTCCCGTGCT GGA CTCCGAC
40 1351 GGCTCCTTCT TCCTCTACAG CAGGCTAACC GTGGACAAGA GCAGGTGGCA
1401 GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC
1451 ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG
45 1501 CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG
1551 CACGTACCCC GTCTACATAC TTCCAGGCA CCCAGCATGG AAATAAAGCA
50 1601 CCCACCACTG CCCTGGGCCC CTGTGAGACT GTGATGGTTC TTTCCACGGG
1651 TCAGGCCGAG TCTGAGGCCT GAGTGACATG AGGGAGGCAG AGCGGTCCCA
1701 CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT CCTCTGC

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SEQ ID NO:26

1 MGWSCIIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT
5 51 EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ
101 GLRAMDTGLY ICKVELMYPP PYYLIGINGT QIYVIDPEPC PDSDQESKYG
10 151 PPSPSSPAPE FEGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDV SQEDPEV
201 QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV SVLTVLHQDW LNGKEYKCKV
251 SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV SLTCLVKGFY
15 301 PSDIAVEWES NGQPENNYKT TPPVLDS DGS FFLYSRLTVD KSRWQEGNVF
351 SCSVMHEALH NHYTQKSLSL SLGK*

SEQ ID NO: 27

20 1 CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT
51 GAGCACACAG GACCTACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG
25 101 TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA
151 CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG
30 201 TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC
251 CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC
301 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG
35 351 TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT
401 TCATCTGCA CGGGCACCTC CAGTGAAAT CAAGTGAACC TCACTATCCA
40 451 AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA
501 TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAAC CCAGATTTAT
551 GTAATTGATC CAGAACCGTG CCCAGATTCT GATCAGGAGT CCAAATATGG
45 601 TCCCCCATCC CCATCATCCC CAGGTAAGCC AACCCAGGCC TCGCCCTCCA
651 GCTCAAGGCG GGACAGGTGC CCTAGAGTAG CCTGCATCCA GGGACAGGCC
701 CCAGCCGGGT GCTGACGCAT CCACCTCCAT CTCTTCCTCA GCACCTGAGT
50 751 TCGAGGGGGC ACCATCAGTC TTCCTGTTCC CCCC AAAACC CAAGGACACT
801 CTCATGATCT CCCGGACCCC TGAGGTCACG TCGTGTTGG TGGACGTGAG

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851 CCAGGAAGAC CCCGAGGTCC AGTTCAACTG GTACGTGGAT GGCGTGGAGG
901 TGCATAATGC CAAGACAAAG CCGCGGGAGG AGCAGTTCAA CAGCACGTAC
5 951 CGTGTGGTCA GCGTCCTCAC CGTCCTGCAC CAGGACTGGC TGAACGGCAA
1001 GGAGTACAAG TGCAAGGTCT CCAACAAAGG CCTCCCGTCC TCCATCGAGA
1051 AAACCATCTC CAAAGCCAAA GGTGGGACCC ACGGGGTGCG AGGGCCACAC
10 1101 GGACAGAGGC CAGCTCGGCC CACCCTCTGC CCTGGGAGTG ACCGCTGTGC
1151 CAACCTCTGT CCCTACAGGG CAGCCCCGAG AGCCACAGGT GTACACCCTG
15 1201 CCCCCATCCC AGGAGGAGAT GACCAAGAAC CAGGTCAGCC TGACCTGCCT
1251 GGTCAAAGGC TTCTACCCCA GCGACATCGC CGTGGAGTGG GAGAGCAATG
1301 GGCAGCCGGA GAACAACTAC AAGACCACGC CTCCCGTGCT GGA CTCCGAC
20 1351 GGCTCCTTCT TCCTCTACAG CAGGCTAACC GTGGACAAGA GCAGGTGGCA
1401 GGAGGGGAAT GTCTTCTCAT GCTCCGTGAT GCATGAGGCT CTGCACAACC
25 1451 ACTACACACA GAAGAGCCTC TCCCTGTCTC TGGGTAAATG AGTGCCAGGG
1501 CCGGCAAGCC CCCGCTCCCC GGGCTCTCGG GGTCGCGCGA GGATGCTTGG
1551 CACGTACCCC GTCTACATAC TTCCCAGGCA CCCAGCATGG AAATAAAGCA
30 1601 CCCACCACTG CCCTGGGCCC CTGTGAGACT GTGATGGTTC TTTCCACGGG
1651 TCAGGCCGAG TCTGAGGCCT GAGTGACATG AGGGAGGCAG AGCGGTCCCA
35 1701 CTGTCCCCAC ACTGGGGATC CCCGGGTACC GAGCTCGATT CCTCTGC

SEQ ID NO:28

1 MGWSCIIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT
40 51 EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ
101 GLRAMDTGLY ICKVELMYPP PYYLGIGNGT QIYVIDPEPC PDSQESKYG
45 151 PPSPSSPAPE FEGAPSVFLF PPKPKDTLMI SRTPEVTCVV VDV SQEDPEV
201 QFNWYVDGVE VHNAKTKPRE EQFNSTYRVV SVLTVLHQDW LNGKEYKCKV
251 SNKGLPSSIE KTISKAKGQP REPQVYTLPP SQEEMTKNQV SLTCLVKGFY
50 301 PSDIAVEWES NGQPENNYKT TPPVLDSGGS FFLYSRLTVD KSRWQEGNVF
351 SCSVMHEALH NHYTQKSLSL SLGK*

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SEQ ID NO: 29

1 CATTTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT
5 51 GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG
101 TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA
151 CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG
10 201 TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC
251 CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC
15 301 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG
351 TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT
401 TCCATCTGCA CGGGCACCTC CAGTGGAAT CAAGTGAACC TCACTATCCA
20 451 AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA
501 TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC CCAGATTTCA
25 551 GGTGAGTCCT TACAACCTCT CTCTTCTATT CAGCTTAAAT AGATTTTACT
601 GCATTTGTTG GGGGGGAAAT GTGTGTATCT GAATTTGAGG TCATGAAGGA
651 CTAGGGACAC CTTGGGAGTC AGAAAGGGTC ATTGGGAGCC CGGGCTGATG
30 701 CAGACAGACA TCCTCAGCTC CCAGACTTCA TGGCCAGAGA TTTATAGTCT
751 AGAGGATCCC CAGCTTTCTG GGGCAGGCCA GGCCTGACCT TGGCTTTGGG
35 801 GCAGGGAGGG GGCTAAGGTG AGGCAGGTGG CGCCAGCAGG TGCACACCCA
851 ATGCQCATGA GCCCAGACAC TGGACGCTGA ACCTCGCGGA CAGTTAAGAA
901 CCAGGGGCC TCTGCGCCTG GGCCAGCTC TGTCCACAC CGCGGTCACA
40 951 TGGCACCACC TCTCTTGAG CCTCCACCA GGGCCCATCG GTCTTCCCCC
1001 TGGCACCTC CTCCAAGAGC ACCTCTGGG GCACAGCGGC CCTGGGCTGC
45 1051 CTGGTCAAGG ACTACTTCCC CGAACCAGGTG ACGGTGTCGT GGAAGTCAGG
1101 CGCCCTGACC AGCGGCGTGC ACACCTTCCC GGCTGTCCTA CAGTCCTCAG
1151 GACTCTACTC CCTCAGCAGC GTGGTGACCG TGCCCTCCAG CAGCTTGGGC
50 1201 ACCCAGACCT ACATCTGCAA CGTGAATCAC AAGCCAGCA ACACCAAGGT
1251 GGACAAGAAA GTTGGTGAGA GGCCAGCACA GGGAGGGAGG GTGTCTGCTG
55 1301 GAAGCAGGCT CAGCGCTCCT GCCTGGACGC ATCCCGGCTA TGCAGCCCCA

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1351 GTCCAGGGCA GCAAGGCAGG CCCCCTCTGC CTCTTCACCC GGAGCCTCTG
1401 CCCGCCCCAC TCATGCTCAG GGAGAGGGTC TTCTGGCTTT TTCCCAGGCT
5 1451 CTGGGCAGGC ACAGGCTAGG TGCCCCTAAC CCAGGCCCTG CACACAAAGG
1501 GGCAGGTGCT GGGCTCAGAC CTGCCAAGAG CCATATCCGG GAGGACCCTG
1551 CCCCTGACCT AAGCCCACCC CAAAGGCCAA ACTCTCCACT CCCTCAGCTC
10 1601 GGACACCTTC TCTCCTCCCA GATTCCAGTA ACTCCCAATC TTCTCTCTGC
1651 AGAGCCCAAA TCTTGTGACA AAACCTCACAC ATGCCCACCG TGCCCAGGTA
15 1701 AGCCAGCCCA GGCCTCGCCC TCCAGCTCAA GGCGGGACAG GTGCCCTAGA
1751 GTAGCCTGCA TCCAGGGACA GGCCCCAGCC GGGTGCTGAC ACGTCCACCT
1801 CCATCTCTTC CTCAGCACCT GAACTCCTGG GGGGACCGTC AGTCTTCCTC
20 1851 TTCCCCCAA AACCCAAGGA CACCCTCATG ATCTCCCGGA CCCCTGAGGT
1901 CACATGCGTG GTGGTGGACG TGAGCCACGA AGACCCTGAG GTCAAGTTCA
25 1951 ACTGGTACGT GGACGGCGTG GAGGTGCATA ATGCCAAGAC AAAGCCGCGG
2001 GAGGAGCAGT ACAACAGCAC GTACCGGGTG GTCAGCGTCC TCACCGTCCT
2051 GCACCAGGAC TGGCTGAATG GCAAGGAGTA CAAGTGCAAG GTCTCCAACA
30 2101 AAGCCCTCCC AGCCCCATC GAGAAAACCA TCTCCAAAGC CAAAGGTGGG
2151 ACCCGTGGGG TGCAGGGGCC ACATGGACAG AGGCCGGCTC GGCCCCACCT
35 2201 CTGCCCTGAG AGTGACCGCT GTACCAACCT CTGTCTTACA GGGCAGCCCC
2251 GAGAACCACA GGTGTACACC CTGCCCCCAT CCCGGGATGA GCTGACCAAG
2301 AACCAGGTCA GCCTGACCTG CCTGGTCAAA GGCTTCTATC CCAGCGACAT
40 2351 CGCCGTGGAG TGGGAGAGCA ATGGGCAGCC GGAGAACAAC TACAAGACCA
2401 CGCCTCCCGT GCTGGACTCC GACGGCTCCT TCTTCCTCTA CAGCAAGCTC
45 2451 ACCGTGGACA AGAGCAGGTG GCAGCAGGGG AACGTCTTCT CATGCTCCGT
2501 GATGCATGAG GCTCTGCACA ACCACTACAC GCAGAAGAGC CTCTCCCTGT
2551 CTCCGGGTAA ATGAGTGCGA CGGCCGGCAA GCCCGCTCC CCGGGCTCTC
50 2601 GCGGTCGCAC GAGGATGCTT GGCACGTACC CCCTGTACAT ACTTCCCGG
2651 CGCCCAGCAT GGAAATAAAG CACCCAGCGC TGCCCTGGGC CCCTGCGAGA
55 2701 CTGTGATGGT TCTTTCCACG GGTCAGGCCG AGTCTGAGGC CTGAGTGGA
2751 TGAGGGAGGC AGAGCGGGTC

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SEQ ID NO:30

5 1 MGWSCIIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT
51 EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ
101 GLRAMDTGLY ICKVELMYPP PYYLGIGNGA QITVAAPSVF IFPPSDEQLK
10 151 SGTASVVCLL NNFYPBREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYSLs
201 STLTLKADY EKHKVYACEV THQGLSSPVT KSFNRGEC*

SEQ ID NO: 31

15 1 CATTCGCTTA CCTCGAGAAG CTTGAGATCA CAGTTCTCTC TACAGTTACT
51 GAGCACACAG GACCTCACCA TGGGATGGAG CTGTATCATC CTCTTCTTGG
20 101 TAGCAACAGC TACAGGTAAG GGGCTCACAG TAGCAGGCTT GAGGTCTGGA
151 CATATATATG GGTGACAATG ACATCCACTT TGCCTTTCTC TCCACAGGTG
25 201 TCCACTCCGC AATGCACGTG GCCCAGCCTG CTGTGGTACT GGCCAGCAGC
251 CGAGGCATCG CCAGCTTTGT GTGTGAGTAT GCATCTCCAG GCAAAGCCAC
30 301 TGAGGTCCGG GTGACAGTGC TTCGGCAGGC TGACAGCCAG GTGACTGAAG
351 TCTGTGCGGC AACCTACATG ATGGGGAATG AGTTGACCTT CCTAGATGAT
401 TCCATCTGCA CGGGCACCTC CAGTGGAAT CAAGTGAACC TCACTATCCA
35 451 AGGACTGAGG GCCATGGACA CGGGACTCTA CATCTGCAAG GTGGAGCTCA
501 TGTACCCACC GCCATACTAC CTGGGCATAG GCAACGGAGC CCAGATTAAA
551 CGTGAGTAGA ATTTAAACTT TGCTTCCTCA GTTTCTAGAA GAATGGCTGC
40 601 AAAGAGCTCC AACAAAACAA TTTAGAACTT TATTAAGGAA TAGGGGGAAG
651 CTAGGAAGAA ACTCAAAACA TCAAGATTTT AAATACGCTT CTTGGTCTCC
45 701 TTGCTATAAT TATCTGGGAT AAGCATGCTG TTTTCTGTCT GTCCCTAACA
751 TGCCCTGTGA TTATCCGCAA ACAACACACC CAAGGGCAGA ACTTTGTTAC
801 TTAAACACCA TCCTGTTTGC TTCTTTCCTC AGGAACTGTG GCTGCACCAT
50 851 CTGTCTTCAT CTCCCGCCA TCTGATGAGC AGTTGAAATC TGGAAGTCCC
901 TCTGTTGTGT GCCTGCTGAA TAACTTCTAT CCCAGAGAGG CCAAAGTACA
55 951 GTGGAAGGTG GATAACGCCC TCCAATCGGG TAACTCCCAG GAGAGTGTCA

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5 1001 CAGAGCAGGA CAGCAAGGAC AGCACCTACA GCCTCAGCAG CACCCTGACG
1051 CTGAGCAAAG CAGACTACGA GAAACACAAA GTCTACGCCT GCGAAGTCAC
1101 CCATCAGGGC CTGAGCTCGC CCGTCACAAA GAGCTTCAAC AGGGGAGAGT
1151 GTTAGAGGGA GAAGTGCCCC CACCTGCTCC TCAGTTCCAG CCTGACCCCC
10 1201 TCCCATCCTT TGGCCTCTGA CCCTTTTTC ACAGGGGACC TACCCCTATT
1251 GCGGTCCTCC AGCTCATCTT TCACCTCACC CCCCTCCTCC TCCTTGGCTT
15 1301 TAATTATGCT AATGTTGGAG GAGAATGAAT AAATAAAGTG AATCTTTGCA
1351 CCTGTGGTTT CTCTCTTTCC TCAATTTAAT AATTATTATC TGTGTTTAC
1401 CAACTACTCA ATTTCTCTTA TAAGGGACTA AATATGTAGT CATCCTAAGG
20 1451 CGCATAACCA TTTATAAAAA TCATCCTTCA TTCTATTTTA CCCTATCATC
1501 CTCTGCAAGA CAGTCCTCCC TCAAACCCAC AAGCCTTCTG TCCTCACAGT
25 1551 CCCCTGGGCC GTGGTAGGAG AGACTTGCTT CCTTGTTTTT CCCTCCTCAG
1601 CAAGCCCTCA TAGTCCTTTT TAAGGGTGAC AGGTCTTACG GTCATATATC
1651 CTTTGATTCA ATTCCCTGGG AATCAACCAA GGCAAATTTT TCAAAAGAAG
30 1701 AAACCTGC

SEQ ID NO:32

35 1 MGWSCIILFL VATATGVHSA MHVAQPAVVL ASSRGIASFV CEYASPGKAT
51 EVRVTVLRQA DSQVTEVCAA TYMMGNELTF LDDSICTGTS SGNQVNLTIQ
101 GLRAMDTGLY ICKVELMYPP PYYLGIGNGA QITVAAPSVF IFPPSDEQLK
40 151 SGTASVVCLL NNFYPREAKV QWKVDNALQS GNSQESVTEQ DSKDSTYLS
201 STLTLKADY EKHKVYACEV THQGLSSPVT KSFNRGEC*